REMARKS

Claims 34 and 35-81 are pending. Independent Claim 34 has been revised to describe 90% identical sequences by reference to SEQ ID NO: 2 instead of to a fragment of SEQ ID NO: 2. Claim 36 has been revised similarly. Claims 38, 39, 54, and 59 have been revised to correct typographical errors or for clarity. Claims 70, 72 and 73 have been amended to correct dependency. Accordingly, the Applicants do not believe that any new matter has been added.

The Applicants thank Examiner Hutson for the discussions in July and August related to avoiding the remaining description and enablement rejections by removing language pertaining to comparison of sequence identity to fragments of SEQ ID NO: 2.

Claim Objections

Claims 37-39, 45, 49, 54 and 80 were objected to as depending from rejected Claim 34 or for various informalities. The Applicants submit that this objection is moot in view of the amendments above.

Rejections--35 U.S.C. 112, first paragraph

Claims 34, 36, 40-44, 46-48, 50-53, 55, 63-79 were rejected under 35 U.S.C. 112, first paragraph, as lacking adequate description. The Applicants submit that these rejections are now moot. The concern was that while the specification supports fragments of SEQ ID NO: 2 and sequences which encode polypeptides at least 90% identical to SEQ ID NO: 2, that it did not provide adequate descriptive support for a polypeptide that was at least 90% identical to a fragment of SEQ ID NO: 2.

Claim 34 now has been revised to refer to a polypeptide that is at least 90% identical to SEQ ID NO: 2 and remove the language pertaining to comparison of sequence identity

with fragments of SEQ ID NO: 2. Accordingly, the Applicants respectfully request that this rejection be withdrawn.

Rejections--35 U.S.C. 112, first paragraph

Claims 34, 36, 40-44, 46-48, 50-53, 55, 63-79 and 81 were rejected under 35 U.S.C. 112, first paragraph, as lacking adequate enablement. This rejection is moot because based on the state of the art in molecular biology as well as on the guidance provided by the specification it would not require undue experimentation to make and use a polynucleotide that encodes a polypeptide having at least 90% identity to SEQ ID NO:2 or a fragment of such a polypeptide that has methylene tetrahydrofolate reductase activity.

Once a coding sequence (e.g., SEQ ID NO: 1; specification, page 7, line 7) or the actual or deduced amino acid sequence of an encoded polypeptide (e.g., SEQ ID NO: 2, page 7, line 22) is known, it is routine to make fragments of either the polynucleotide or of the polypeptide it encodes. The polypeptides encoded by such a polynucleotide can be routinely assayed for an enzymatic activity, such as tetrahydrofolate reductase activity [EC: 1.7.99.5] (specification, page 6, line 8). Moreover, the specification exemplifies the identification of a *metF* gene, its cloning and transformation into a host cell, and the subsequent ability of the transformed cells to produce high amounts of methionine, see e.g., Examples 2-4 on pages 20-26 and Table 1 on page 26 of the specification. Accordingly, the Applicants respectfully submit that this rejection may be withdrawn.

CONCLUSION

In view of the above amendments and remarks, the Applicants respectfully submit that this application is now in condition for allowance. Early notification to that effect is earnestly solicited.

Respectfully submitted,

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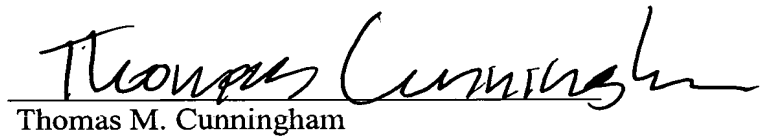
Norman F. Oblon



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